Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	12	"6673616".pn. or "6372424".pn. or "5843654".pn. or "5888780".pn. or "5719028".pn. or "5614402".pn. or "5541311".pn. or "5422253".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L2	8566	Sequence WITH targeting	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L3	43	(Sequence WITH targeting) SAME oligo	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L4	3203	sequence WITH labeling	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L5	0	(sequence WITH labeling) SAME oligonu	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L6	1000	(sequence WITH labeling) and oligo	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L7	65	(sequence WITH labeling) SAME oligo	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L8	49	(sequence WITH labeling) SAME fluorophore	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L9	57436	biotin or radiolabel or hapten or chormophore	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L10	4263	(biotin or radiolabel or hapten or chormophore) and (Sequence WITH targeting)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L11	2120	((biotin or radiolabel or hapten or chormophore) and (Sequence WITH targeting)) and oligo	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46

L12	27	l11 and "solid support"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L13	363	(((biotin or radiolabel or hapten or chormophore) and (Sequence WITH targeting)) and oligo) and hairpin	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L14	253	((((biotin or radiolabel or hapten or chormophore) and (Sequence WITH targeting)) and oligo) and hairpin) and "target nucleic acid"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L15	0	"mojdeh bahar"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L16	415	bahar	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L17	29	bahar SAME mojdeh	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L18	5281	triplex SAME (nucleic or DNA)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L19	66	(triplex SAME (nucleic or DNA)) SAME oligo	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L20	2	"6410241".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L21	6	"5614401".pn. or "5541311".pn. or "5422253".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L22	6	"5614402".pn. or "5541311".pn. or "5422253".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L23	8	"5614402".pn. or "5541311".pn. or "5422253".pn. or "5719028".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46

L24	2	"6673616".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L25	66	"3' arm" SAME hairpin	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L26	14053	hairpin	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L27	25213	"target DNA" or "target nucleic acid"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L28	6790	"3' arm"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L29	30569	"3' region" or "3' portion"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L30	11336	fluorophore	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L31	50728	"solid support" or "solid matrix"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L32	2417	"third oligonucleotide" or "third probe" or "third primer"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L33	361265	biotin or radiolabel or hapten or chromophore or dye	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L34	34	hairpin and ("target DNA" or "target nucleic acid") and "3' arm" and ("3' region" or "3' portion") and fluorophore and ("solid support" or "solid matrix") and ("third oligonucleotide" or "third probe" or "third primer") and (biotin or radiolabel or hapten or chromophore or dye)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46

L35	68	hairpin and ("target DNA" or "target nucleic acid") and "3' arm"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L36	2	"5541311".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L37	27420	hybridization SAME detection	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L38	1001	(hybridization SAME detection) and ("third oligonucleotide" or "third probe" or "third primer")	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L39	298	((hybridization SAME detection) and ("third oligonucleotide" or "third probe" or "third primer")) and "first oligonucleotide"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:46
L40	2	"5422253".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:52
L41	2	"5541311".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 08:58
L42	2	"6673616".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 09:02
L43	2	"6372424".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 09:14
L44	10	"6673616".pn. or "6372424".pn. or "5843654".pn. or "5888780". pn. or "5719028".pn. or "5614402".pn. or "5541311".pn.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 09:15
L45	707	l10 and hairpin	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 09:16
L46	7	l44 and hairpin	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 09:16

L47	0	l46 and "third oligo"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 09:16
L48	7	l46 and "third"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/01/24 09:17

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 FILE 'MEDLINE, EMBASE, BIOSIS, CAPLUS' ENTERED AT 09:41:53 ON 24 JAN 2005
L1       317188 S DAHLBERG?/AU OR BROW?/AU OR LYAMICHEV?/AU
L2        17436 S THIRD (P) (OLIGONUCLEOTIDE OR FRAGMENT OR PRIMER OR PROBE)
L3        23805 S HAIRPIN
L4            1 S L1 AND L2 AND L3
L5       299343 S (SEQUENCE OR MUTATION OR MUTANT OR "NUCLEIC ACID" OR TARGET)
L6         2634 S L1 AND L5
L7           28 S L6 AND L2
L8           13 DUP REM L7 (15 DUPLICATES REMOVED)
L9          408 S DUPLEX AND L2
L10          38 S L9 AND L3
L11           4 S L10 AND L5
L12           4 DUP REM L11 (0 DUPLICATES REMOVED)
L13           1 S L7 AND L3
L14      519897 S BIOTIN OR HAPTEN OR CHROMOPHORE OR DYE OR RADIOLABEL
L15          45 S L14 AND L6
L16           2 S L15 AND L3
L17           2 DUP REM L16 (0 DUPLICATES REMOVED)
L18         305 S DUPLEX (P) (THIRD (S) OLIGO?)
L19          16 S L18 AND HAIRPIN
L20          11 DUP REM L19 (5 DUPLICATES REMOVED)
L21           5 S L20 NOT PY>=1996
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ANSWER 1 OF 13 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:995892 CAPLUS
DOCUMENT NUMBER: 141:420957
TITLE: Oligonucleotides comprising a molecular switch and their use in hybridization processes, particularly for identification of single base mismatches
INVENTOR(S): Arnold, Lyle J.; **Brown, Bob D.**
PATENT ASSIGNEE(S): Gen-Probe Incorporated, USA
SOURCE: PCT Int. Appl., 57 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004098386	A2	20041118	WO 2004-US13515	20040430

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2003-467517P P 20030501

AB The invention relates to oligonucleotides comprising a mol. switch which may exist in an "open" or "closed" position. The mol. switch region can be in an "open" (non-hybridized) or "closed" (hybridized) position while the **oligonucleotide** as a whole remains in part hybridized to the target sequence. The mol. switch portion of the **probe** is particularly sensitive to the identity of sequences complementary to the mol. switch. Oligonucleotides containing a mol. switch are applicable to all kinds of hybridization processes. Due to the sensitivity of the switch domain of the **oligonucleotide**, probes containing a mol. switch are particularly useful in the identification of single point mismatches. More specifically, a portion, but not all, of the **oligonucleotide** becomes unbound from a mismatched target. The invention further relates to methods of using said oligonucleotides as hybridization probes or primers, for research reagents and clin. diagnostics. An exemplary **oligonucleotide** comprises a first hybridizable domain, a second bridging block domain, and a **third** binding domain. The examples show melting curves using probes to **detect** wild-type and **mutant target** sequences in the human hemochromatosis gene.

L8 ANSWER 2 OF 13 EMBASE COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 2003081843 EMBASE
TITLE: Molecular characterization of bovine enteric caliciviruses: A distinct third genogroup of noroviruses (Norwalk-like viruses) unlikely to be of risk to humans.
AUTHOR: Oliver S.L.; Dastjerdi A.M.; Wong S.; El-Attar L.; Gallimore C.; **Brown D.W.G.**; Green J.; Bridger J.C.
CORPORATE SOURCE: J.C. Bridger, Department of Pathology, Royal Veterinary College, Royal College St., London NW1 OTU, United Kingdom. jbridger@rvc.ac.uk

SOURCE: Journal of Virology, (2003) 77/4 (2789-2798).
Refs: 48
ISSN: 0022-538X CODEN: JOVIAM
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Bovine enteric caliciviruses (BoCVs) have been classified in the Norovirus (Norwalk-like virus) genus of the Caliciviridae, raising questions about zoonotic transmission and an animal reservoir for the human Norwalk-like viruses (NLVs), an important cause of nonbacterial gastroenteritis in humans. We examined the genetic relationship of human NLVs to BoCVs that were identified by using reverse transcription-PCR with **primer** pairs originally designed to **detect** human NLVs. Polymerase, capsid, and open reading frame 3 (ORF3) gene **sequence** analyses of BoCVs that were identified from 1976 to 2000 from throughout the United Kingdom showed that BoCVs formed a distinct **third** genogroup of closely related viruses distinct from the human genogroup I and II NLVs. Evidence was not obtained to support the concept that BoCVs are circulating in humans and pose a threat to human health.

L8 ANSWER 3 OF 13 EMBASE
on STN
ACCESSION NUMBER: 2001104953 EMBASE
TITLE: Identification of intrinsic order and disorder in the DNA repair protein XPA.
AUTHOR: Iakoucheva L.M.; Kimzey A.L.; Masselon C.D.; Bruce J.E.; Garner E.C.; **Brown C.J.**; Keith Dunker A.; Smith R.D.; Ackerman E.J.
CORPORATE SOURCE: E.J. Ackerman, PNNL, Molecular Biosciences Department, P.O. Box 999, Richland, WA 99352, United States.
eric.ackerman@pnl.gov
SOURCE: Protein Science, (2001) 10/3 (560-571).
Refs: 50
ISSN: 0961-8368 CODEN: PRCIEI
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The DNA-repair protein XPA is required to recognize a wide variety of bulky lesions during nucleotide excision repair. Independent NMR solution structures of a human XPA **fragment** comprising approximately 40% of the full-length protein, the minimal DNA-binding domain, revealed that one-**third** of this molecule was disordered. To better characterize structural features of full-length XPA, we performed time-resolved trypsin proteolysis on active recombinant Xenopus XPA (xXPA). The resulting proteolytic fragments were analyzed by electrospray ionization interface coupled to a Fourier transform ion cyclotron resonance mass spectrometry and SDS-PAGE. The molecular weight of the full-length xXPA determined by mass spectrometry (30922.02 daltons) was consistent with that calculated from the **sequence** (30922.45 daltons). Moreover, the mass spectrometric data allowed the assignment of multiple xXPA fragments not resolvable by SDS-PAGE. The neural network program Predictor of Natural Disordered Regions (PONDR) applied to xXPA predicted extended disordered N- and C-terminal regions with an ordered internal core. This prediction agreed with our partial proteolysis results, thereby indicating that disorder in XPA shares **sequence** features with other well-characterized intrinsically unstructured proteins. Trypsin cleavages at 30 of the possible 48 sites were **detected** and no **cleavage** was observed in an internal

region (Q85-I179) despite 14 possible cut sites. For the full-length xXPA, there was strong agreement among PONDR, partial proteolysis data, and the NMR structure for the corresponding XPA **fragment**.

L8 ANSWER 4 OF 13 EMBASE COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 2000363779 EMBASE
TITLE: A bead-based method for multiplexed identification and quantitation of DNA sequences using flow cytometry.
AUTHOR: Spiro A.; Lowe M.; **Brown D.**
CORPORATE SOURCE: M. Lowe, Physics Department, Loyola College in Maryland, Baltimore, MD 21210, United States. mlowe@loyola.edu
SOURCE: Applied and Environmental Microbiology, (2000) 66/10 (4258-4265).
Refs: 22
ISSN: 0099-2240 CODEN: AEMIDF
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English
AB A new multiplexed, bead-based method which utilizes **nucleic acid** hybridizations on the surface of microscopic polystyrene spheres to identify specific sequences in heterogeneous mixtures of DNA sequences is described. The method consists of three elements: beads (5.6-μm diameter) with oligomer capture probes attached to the surface, three fluorophores for multiplexed **detection**, and flow cytometry instrumentation. Two fluorophores are impregnated within each bead in varying amounts to create different bead types, each associated with a unique **probe**. The **third** fluorophore is a reporter. Following capture of fluorescent cDNA sequences from environmental samples, the beads are analyzed by flow cytometric techniques which yield a signal intensity for each capture **probe** proportional to the amount of **target** sequences in the analyte. In this study, a direct hybrid capture assay was developed and evaluated with regard to **sequence** discrimination and quantitation of abundances. The **target** sequences (628 to 728 bp in length) were obtained from the 16S/23S intergenic spacer region of microorganisms collected from polluted groundwater at the nuclear waste site in Hanford, Wash. A fluorescence standard consisting of beads with a known number of fluorescent DNA molecules on the surface was developed, and the resolution, sensitivity, and lower **detection** limit for measuring abundances were determined. The results were compared with those of a DNA microarray using the same sequences. The bead method exhibited far superior **sequence** discrimination and possesses features which facilitate accurate quantitation.

L8 ANSWER 5 OF 13 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1999:732986 CAPLUS
DOCUMENT NUMBER: 131:347456
TITLE: Invasive **cleavage** of nucleic acids with thermostable 5'-nuclease for **mutation detection** and **diagnostic** applications.
INVENTOR(S): Prudent, James R.; Hall, Jeff G.; **Lyamichev, Victor I.; Brow, Mary Ann D.; Dahlberg, James E.**
PATENT ASSIGNEE(S): Third Wave Technologies, Inc., USA
SOURCE: U.S., 182 pp., Cont.-in-part of U.S. Ser. No. 682,853.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English

FAMILY ACC. NUM. COUNT: 22
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5985557	A	19991116	US 1996-756386	19961126
US 5846717	A	19981208	US 1996-599491	19960124
US 6001567	A	19991214	US 1996-682853	19960712
US 6090606	A	20000718	US 1996-758314	19961202
US 6090543	A	20000718	US 1996-759038	19961202
CA 2243353	AA	19970731	CA 1997-2243353	19970122
WO 9727214	A1	19970731	WO 1997-US1072	19970122
W: AU, CA, JP, US				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9718364	A1	19970820	AU 1997-18364	19970122
AU 731062	B2	20010322		
EP 904286	A1	19990331	EP 1997-903931	19970122
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2002515737	T2	20020528	JP 1997-526989	19970122
US 5994069	A	19991130	US 1997-823516	19970324
US 6348314	B1	20020219	US 1999-350309	19990709
US 6458535	B1	20021001	US 1999-350597	19990709
US 2004018489	A1	20040129	US 2001-864426	20010524
US 2003044796	A1	20030306	US 2001-940244	20010827
US 6692917	B2	20040217		
US 2003096245	A1	20030522	US 2001-982667	20011018
US 2002187486	A1	20021212	US 2001-33297	20011102
US 2002197623	A1	20021226	US 2002-81806	20020222
US 2003186238	A1	20031002	US 2002-84839	20020226
US 2003152971	A1	20030814	US 2002-290386	20021107
US 2004214174	A1	20041028	US 2002-309584	20021204
US 2004072182	A1	20040415	US 2003-356861	20030203

PRIORITY APPLN. INFO.:

US 1996-599491	A2	19960124
US 1996-682853	A2	19960712
US 1995-381212	A2	19950131
US 1996-756038	B2	19961126
US 1996-756386	A2	19961126
US 1996-758314	A2	19961202
US 1996-759038	A2	19961202
WO 1997-US1072	W	19970122
US 1997-823516	A1	19970324
WO 1998-US5809	W	19980324
US 1999-350309	A2	19990709
US 1999-350597	A1	19990709
US 2000-381212	A2	20000208
US 2000-577304	A2	20000524
US 2000-713601	A2	20001115
US 2000-732622	A2	20001208
US 2001-758282	A2	20010111
US 2001-864636	A2	20010524
US 2001-982667	A1	20011018
US 2001-344946P	P	20011107
US 2002-361060P	P	20020227
US 2002-290386	A2	20021107

AB The present invention relates to means for the **detection** and characterization of **nucleic acid** sequences, as well as variations in **nucleic acid** sequences. The present invention also relates to methods for forming a **nucleic acid cleavage** structure on a **target sequence** and cleaving the **nucleic acid cleavage** structure in a site-specific manner. The

structure-specific 5'-nuclease activity of a variety of enzymes is used to cleave the **target**-dependent **cleavage** structure, thereby indicating the presence of specific **nucleic acid** sequences or specific variations thereof. These 5'-nucleases are capable of cleaving linear duplex structures to create single discrete cleavage products identified using fluorescence imaging. The reaction involves a trigger and a detection reaction where a hairpin conformation is recognized. Here the target nucleic acid is not completely complementary to at least one of the first, second, **third** and fourth oligonucleotides. Assays where the **target nucleic acid** is reused or recycled during multiple rounds of hybridization with **oligonucleotide** probes and **cleavage** without the need to use temperature cyclin or **nucleic acid** synthesis. Through the interaction of the **cleavage** means an upstream **oligonucleotide** can be made to cleave a downstream **oligonucleotide** at an internal site in such a way that the resulting fragments of the downstream **oligonucleotide** dissociated from the **target nucleic acid**, thereby making that region of the **target nucleic acid** available for hybridization to another, uncleaved copy of the downstream **oligonucleotide**. The specific stability designed into the invader and **probe** sequences will depend on the temperature at which one desires to perform the reaction. It is desirable that the invader **oligonucleotide** be immediately available to direct the **cleavage** of each **probe oligonucleotide** that hybridizes to a **target nucleic acid**. For this reason, the invader **oligonucleotide** is provided in excess over the **probe oligonucleotide**. The non-**target cleavage** products are incubated with a template-independent polymerase and one nucleoside triphosphate under conditions such that at least one nucleotide is added to the 3'-hydroxyl group of the non-**target cleavage** products to generate tailed products. The present invention also provides novel methods and devices for the separation of nucleic acid mols. by charge by charge reversal. When an **oligonucleotide** is shortened through the action of a CLEAVASE enzyme or other cleavage agent, the pos. charge can be made to not only significantly reduce the net neg. charge, but to actually override it, effectively "flipping" the net charge of the labeled entity. The reversal of charge allows the products of **target**-specific **cleavage** to be partitioned from uncleaved **probe** by extremely simple means. It has clin. diagnostic applications as multiple alleles could be screened at once.

REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 6 OF 13 MEDLINE on STN DUPLICATE 1

ACCESSION NUMBER: 1999452716 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10521282
TITLE: DNA triple helix formation at target sites containing several pyrimidine interruptions: stabilization by protonated cytosine or 5-(1-propargylamino)dU.
AUTHOR: Gowers D M; Bijapur J; **Brown T**; Fox K R
CORPORATE SOURCE: Division of Biochemistry and Molecular Biology, School of Biological Sciences, University of Southampton, U.K.
SOURCE: Biochemistry, (1999 Oct 12) 38 (41) 13747-58. Journal code: 0370623. ISSN: 0006-2960.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199911
ENTRY DATE: Entered STN: 20000111

Last Updated on STN: 20000111
Entered Medline: 19991117

AB DNase I footprinting has been used to study the formation of parallel triplexes at oligopurine target sequences which are interrupted by pyrimidines at regular intervals. TA interruptions are targeted with **third** strand oligonucleotides containing guanine, generating G x TA triplets, while CG base pairs are targeted with thymine, forming T x CG triplets. We have attempted to optimize the stability of these complexes by varying the base composition and sequence arrangement of the target sites, and by replacing the **third** strand thymines with the positively charged analogue 5-(1-propargylamino)dU (U(P)). For the **target sequence** (AAAT)(5)AA, in which pyrimidines are positioned at every fourth residue, triplex formation with TG-containing oligonucleotides is only **detected** in the presence of a triplex-binding ligand, though stable triplexes were **detected** at the **target** site (AAAAAT)(3)AAAA. Triplex stability at targets containing pyrimidines at every fourth residue is increased by introducing guanines into the duplex repeat unit using the targets (AGAT)(5)AA and (ATGA)(5)AA. In contrast, placing C(+) x GC triplets on the 5'-side of G x TA, using the target (AGTA)(5)TT, produces complexes of lower stability. We have attempted further to increase the stability of these complexes by using the positively charged thymine base analogue U(P), and have shown that (TU(P)TG)(5)TT forms a more stable complex with target (AAAT)(5)AA than the unmodified **third** strand, generating a footprint in the absence of a triplex-binding ligand. Triplex formation at (AGTA)(5)AA is improved by using the modified **oligonucleotide** (TCGU(P))(5)TT, generating a complex in which the charged triplets C(+) x GC and U(P) x AT alternate with uncharged triplets. In contrast, placing U(P) x AT triplets adjacent to C(+) x GC, using the **third** strand **oligonucleotide** (U(P)CGT)(5)TT, reduces triplex formation, while the **third** strand with both substitutions, (U(P)CGU(P))(5)TT, produces a complex with intermediate stability. It appears that, although adjacent U(P) x AT triplets form stable triplexes, placing U(P) x AT adjacent to C(+) x GC is unfavorable. Similar results were obtained with fragments containing CG inversions within the oligopurine tract, though triplexes at (AAAAAC)(3)AA were only detected in the presence of a triplex-binding ligand. Placing C(+) x GC on the 5'-side of T x CG triplets also reduces triplex formation, while a 3'-C(+) x GC produces complexes with increased stability.

L8 ANSWER 7 OF 13 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 97278326 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9131633
TITLE: Developmental analysis of factors binding to the mouse 68-kDa neurofilament promoter.
AUTHOR: Kure R; **Brown I R**
CORPORATE SOURCE: Department of Zoology, University of Toronto, West Hill Ontario, Canada.
SOURCE: Neurochemical research, (1997 May) 22 (5) 555-62. Journal code: 7613461. ISSN: 0364-3190.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199706
ENTRY DATE: Entered STN: 19970709
Last Updated on STN: 19970709
Entered Medline: 19970620

AB Whole tissue extracts prepared from mouse brain regions at various postnatal ages were characterized for binding of factors to the DNase I hypersensitive site (HSSI) which is located closest to the transcription start site of the 68-kDa mouse neurofilament gene (NF-L). Gel mobility

shift assays detected changes in factor binding during postnatal development of the neocortex. Competition experiments suggested that one of the complexes resulted from factor binding to a 9 bp sequence found in both the light and medium neurofilament promoter regions (NF-L/M). Gel mobility shifts performed with an **oligonucleotide probe** containing the NF-L/M **sequence detected** two brain-specific DNA-protein complexes, and a **third** complex in both brain and liver. During cerebellar and neocortical development, one of the NF-L/M complexes was most intense at postnatal day 10 when transcription of the NF-L gene is upregulated.

L8 ANSWER 8 OF 13 MEDLINE on STN DUPLICATE 3
ACCESSION NUMBER: 96332521 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8760431
TITLE: Common epitope on protein VI of enteric adenoviruses from subgenera A and F.
AUTHOR: Grydsuk J D; Fortsas E; Petric M; **Brown M**
CORPORATE SOURCE: Department of Microbiology, University of Toronto, Ontario, Canada.
SOURCE: Journal of general virology, (1996 Aug) 77 (Pt 8) 1811-9. Journal code: 0077340. ISSN: 0022-1317.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U14651; GENBANK-U14652; GENBANK-U14653
ENTRY MONTH: 199609
ENTRY DATE: Entered STN: 19960924
Last Updated on STN: 19980206
Entered Medline: 19960918

AB Western blot analysis with monoclonal antibodies, produced in response to immunization with gradient-purified adenovirus 41 (Ad41) virions, identified two epitopes of interest on protein VI of enteric adenoviruses. One epitope is unique to subgenus F adenoviruses (Ad40 and Ad41); the other epitope is common to subgenus A (Ad12, 18 and 31) and subgenus F(Ad40, 41) adenoviruses but is not shared by representative serotypes of subgenera B (Ad3 and 7), C(Ad1, 2 and 5), D(Ad8) or E (Ad4). Alignment of the deduced amino acid sequence of the genes encoding the protein VI precursor (pre-VI) of Ad40 and Ad41 (subgenus F), Ad12 and Ad31 (subgenus A), Ad2 and Ad5 (subgenus C) shows that the N-terminal one-**third** and C-terminal 23 amino acids of pre-VI are highly conserved. Within the central domain, pre-VI of subgenus F serotypes is more closely related to that of subgenus A serotypes than to pre-VI of the non-enteric subgenus C adenoviruses (Ad2 and Ad5). By expressing random **oligonucleotide** fragments of the Ad41 protein VI gene as part of a T7 gene 10 fusion protein, the two epitopes of interest were mapped to within the same 14 amino acid region in the central domain of protein VI. Given the association of subgenera A and F adenoviruses with paediatric gastroenteritis, the epitope shared by these serotypes may be functionally significant with respect to gut tropism. In addition, this epitope is potentially valuable as a **target** for the **detection** of enteric adenoviruses in clinical specimens.

L8 ANSWER 9 OF 13 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 95297143 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7778277
TITLE: Characterisation and mutational analysis of an ORF 1a-encoding proteinase domain responsible for proteolytic processing of the infectious bronchitis virus 1a/1b polyprotein.
AUTHOR: Liu D X; **Brown T D**
CORPORATE SOURCE: Department of Pathology, University of Cambridge, United

Kingdom.
SOURCE: Virology, (1995 Jun 1) 209 (2) 420-7.
Journal code: 0110674. ISSN: 0042-6822.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199507
ENTRY DATE: Entered STN: 19950720
Last Updated on STN: 20000303
Entered Medline: 19950711

AB Coronavirus gene expression involves proteolytic processing of the mRNA 1-encoded polyproteins by viral and cellular proteinases. Recently, we have demonstrated that an ORF 1b-encoded 100-kDa protein is proteolytically cleaved from the 1a/1b fusion polyprotein by a viral-specific proteinase of the picornavirus 3C proteinase group (3C-like proteinase). In this report, the 3C-like proteinase has been further analysed by internal deletion of a 2.3-kb **fragment** between the 3C-like proteinase-encoding region and ORF 1b and by substitution mutations of its catalytic centre as well as the two predicted cleavage sites flanking the 100-kDa protein. The results show that internal deletion of ORF 1a sequences from nucleotide 9911 to 12227 does not influence the catalytic activity of the proteinase in processing of the 1a/1b polyprotein to the 100-kDa protein species. Site-directed mutagenesis studies have confirmed that the predicted nucleophilic cysteine residue (Cys2922) and a histidine residue encoded by ORF 1a from nucleotide 8985 to 8987 (His2820) are essential for the catalytic activity of the proteinase, and that the QS(G) dipeptide bonds are its **target cleavage** sites. Substitution mutations of the **third** component of the putative catalytic triad, the glutamic acid 2843 (Glu2843) residue, however, do not affect the processing to the 100-kDa protein. In addition, cotransfection experiment shows that the 3C-like proteinase is capable of trans-cleavage of the 1a/1b polyprotein. These studies have confirmed the involvement of the 3C-like proteinase domain in processing of the 1a/1b polyprotein, the predicted catalytic centre of the proteinase, and its cleavage sites.

L8 ANSWER 10 OF 13 EMBASE
on STN
ACCESSION NUMBER: 94187341 EMBASE
DOCUMENT NUMBER: 1994187341
TITLE: Microgonotropens and their interaction with DNA. 4. Synthesis of the tripyrrole peptides tren-microgonotropen-a and -b and characterization of their interactions with dsDNA.
AUTHOR: He G.-X.; **Browne K.A.**; Blasko A.; Bruice T.C.
CORPORATE SOURCE: Department of Chemistry, University of California, Santa Barbara, CA 93106, United States
SOURCE: Journal of the American Chemical Society, (1994) 116/9 (3716-3725).
ISSN: 0002-7863 CODEN: JACSAT
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 016 Cancer
029 Clinical Biochemistry
030 Pharmacology
037 Drug Literature Index
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The novel concept of attaching a connector to a pyrrole nitrogen of a tripyrrole peptide minor groove binding agent to carry functionalities to the phosphates and major groove of DNA has been extended with the

synthesis of tren-microgonotropen-a and -b {6a and 6b; Chart 1}. The tren-microgonotropens are tripeptides of 3-aminopyrrole-2-carboxylic acid where (i) the amino terminus is acetylated; (ii) the terminal carboxyl has an amide linkage to β-(N,N-dimethylamino)propylamine; (iii) the ring nitrogens of the first and **third** pyrrole rings are N-methylated; and (iv) the ring nitrogen of the central pyrrole carries the substituents -(CH2)3NH(CH2)2N{(CH2)2NH2}2 (6a) and -(CH2)4NH(CH2)2N{(CH2)2NH2}2 (6b). To determine the **sequence** specificity of binding, complementary strand analysis by DNase 1 footprinting of 6a,b bound to the 5'- and 3'-[32P] labeled 167 bp EcoRI/RsaI restriction **fragment** of pBR322 was carried out. Results show clear and specific **cleavage** inhibition patterns at three of the four potential A + T-rich binding sites. Employing Hoechst 33258 (Ht) as a fluorescent titrant, the equilibrium constants for the binding of 6a,b to the hexadecameric duplex d(GGCGCAAATTTGGCGG)/d(CCGCCAAATTTGCGCC) were determined (35°C). The equilibrium constants for the formation of 1:1 (K(L)1) and 2:1 (K(L)2) complexes with 6a,b and 5a-c (the dien-microgonotropens) exhibit a slight degree of cooperativity {K(L)2 > K(L)1}. The product K(L1)K(L)2 was slightly greater for 6a and 6b than for the dien-microgonotropens 5a, 5b, and 5c. In addition, we now show that Ht forms a 1:1 and a 2:1 complex with the hexadecamer not only by fluorescence titration but also by 1H NMR titrations. The electrophoretic mobilities of .diameter.X-174-RF DNA HaeIII restriction fragments complexed to 6a or 6b revealed a much greater conformational change in the DNA fragments than when distamycin (Dm) was bound to the same fragments and about a 2-fold greater change than generated by the dien-microgonotropens. Complete inhibition of mammalian topoisomerase 1 with 30 μM 6b was observed while dien-microgonotropen-b and Dm only partially inhibited topoisomerase 1 at 150 μM. Thus, evidence from equilibrium constants for complexation, electrophoretic mobilities, and topoisomerase 1 assays suggests that 6b alters the conformation of DNA in a manner that is not directly related to the affinity of complexation.

L8 ANSWER 11 OF 13 MEDLINE on STN DUPLICATE 5

ACCESSION NUMBER: 95189915 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7883875
TITLE: Early diagnosis of Lassa fever by reverse transcription-PCR.
AUTHOR: Demby A H; Chamberlain J; **Brown D W**; Clegg C S
CORPORATE SOURCE: Virus Reference Division, Central Public Health Laboratory, London, United Kingdom.
SOURCE: Journal of clinical microbiology, (1994 Dec) 32 (12) 2898-903.
Journal code: 7505564. ISSN: 0095-1137.
PUB. COUNTRY: United States
DOCUMENT TYPE: (CLINICAL TRIAL)
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-J04324
ENTRY MONTH: 199504
ENTRY DATE: Entered STN: 19950425
Last Updated on STN: 19950425
Entered Medline: 19950413

AB We developed a method based on a coupled reverse transcription-PCR (RT-PCR) for the detection of Lassa virus using primers specific for regions of the S RNA segment which are well conserved between isolates from Sierra Leone, Liberia, and Nigeria. The specificity of the assay was confirmed by Southern blotting with a chemiluminescent **probe**. The assay was able to **detect** 1 to 10 copies of a plasmid or an RNA transcript containing the **target sequence**. There was complete concordance between RT-PCR and virus culture for the

detection of Lassa virus in a set of 29 positive and 32 negative serum samples obtained on admission to the hospital from patients suspected of having Lassa fever in Sierra Leone. Specificity was confirmed by the failure of amplification of specific products from serum samples collected from 129 healthy blood donors in Sierra Leone or from tissue culture supernatants from cells infected with related arenaviruses (Mopeia, lymphocytic choriomeningitis, Tacaribe, and Pichinde viruses). Sequential serum samples from 29 hospitalized patients confirmed to have Lassa fever were tested by RT-PCR and for Lassa virus-specific antibodies by indirect immunofluorescence (IF). RT-PCR detected virus RNA in 79% of the patients at the time of admission, comparing favorably with IF, which detected antibodies in only 21% of the patients. Lassa virus RNA was detected by RT-PCR in all 29 patients by the **third** day of admission, whereas antibody was detectable by IF in only 52% of the patients. These results point to an important role for RT-PCR in the management of suspected cases of Lassa fever.

L8 ANSWER 12 OF 13 EMBASE
on STN

ACCESSION NUMBER: 88079744 EMBASE
DOCUMENT NUMBER: 1988079744
TITLE: Multiple crm- mutations in familial hypercholesterolemia. Evidence for 13 alleles, including four deletions.
AUTHOR: Hobbs H.H.; Leitersdorf E.; Goldstein J.L.; **Brown M.S.**; Russell D.W.
CORPORATE SOURCE: Department of Molecular Genetics, The University of Texas Health Science Center at Dallas, Dallas, TX 75235, United States
SOURCE: Journal of Clinical Investigation, (1988) 81/3 (909-917). ISSN: 0021-9738 CODEN: JCINAO
COUNTRY: United States
DOCUMENT TYPE: Journal
FILE SEGMENT: 022 Human Genetics
026 Immunology, Serology and Transplantation
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The low density lipoprotein (LDL) receptors in fibroblasts from 132 subjects with the clinical syndrome of homozygous familial hypercholesterolemia were analyzed by immunoprecipitation with an anti-LDL receptor monoclonal antibody. 16 of the 132 cell strains (12%) synthesized no immunodetectable LDL receptor protein, indicating the presence of two **mutant** genes that failed to produce cross-reacting material (crm- mutations). DNA and mRNA from 15 of the 16 crm- patients, representing 30 crm- genes, were available for further study. Haplotype analysis based on 10 restriction **fragment** length polymorphisms (RFLPs) suggested that the 30 crm- genes represent 13 **mutant** alleles. Four of the alleles produced no mRNA. Three of these four mRNA- alleles had large deletions ranging from 6 to 20 kb that eliminated the promoter region of the gene. The fourth mRNA- allele did not contain any deletion or alteration in the promoter **sequence**; the reason for the mRNA- phenotype was not apparent. Nine alleles were positive for mRNAs, of which three encoded mRNAs of abnormal size. One of the abnormal mRNAs was produced by a gene harboring a deletion, and another was produced by a gene with a complex rearrangement. The **third** abnormal-sized mRNA (3.1 kb larger than normal) was produced by an allele that had no **detectable** alterations as judged by Southern blotting. The other six mRNA+ alleles appeared normal by Southern blotting and produced normal-sized mRNA but no receptor protein. The current studies demonstrate that mRNA analysis coupled with haplotype determination by Southern blot analysis can be used to classify crm- mutations at a genetic locus where multiple alleles exist.

L8 ANSWER 13 OF 13 EMBASE COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN

ACCESSION NUMBER: 86016340 EMBASE
DOCUMENT NUMBER: 1986016340
TITLE: Genetic linkage heterogeneity in the fragile X syndrome.
AUTHOR: **Brown W.T.**; Gross A.C.; Chan C.B.; Jenkins E.C.
CORPORATE SOURCE: New York Office of Mental Retardation and Developmental Disabilities, Institute for Basic Research in Developmental Disabilities, Staten Island, NY 10314, United States
SOURCE: Human Genetics, (1985) 71/1 (11-18).
CODEN: HUGEDQ
COUNTRY: Germany
DOCUMENT TYPE: Journal
FILE SEGMENT: 022 Human Genetics
032 Psychiatry
LANGUAGE: English

AB Genetic linkage between a factor IX DNA restriction **fragment** length polymorphism (RFLP) and the fragile X chromosome marker was analyzed in eight fragile X pedigrees and compared to eight previously reported pedigrees. A large pedigree with apparently full penetrance in all male members showed a high frequency of recombination. A lod score of -7.39 at θ = 0 and a maximum score of 0.26 at θ = 0.32 were calculated. A second large pedigree with a nonpenetrant male showed tight linkage with a maximum lod score of 3.13 at θ = 0, a result similar to one large pedigree with a nonpenetrant male previously reported. The differences in lod score seen in these large pedigrees suggest there was genetic heterogeneity in linkage between families which appeared to relate to the presence of nonpenetrant males. The combined lod score for the three pedigrees with nonpenetrant males was 6.84 at θ = 0. For the 13 other pedigrees without nonpenetrant males the combined lod score was -21.81 at θ = 0, with a peak of 0.98 at θ = 0.28. When lod scores from all 16 families were combined, the value was -15.14 at θ = 0 and the overall maximum was s 5.13 at θ = 0.17. To determine whether genetic heterogeneity was present, three statistical tests for heterogeneity were employed. First, a 'predivided-sample' test was used. The 16 pedigrees were divided into two classes, NP and P, based upon whether or not any nonpenetrant males were **detected** in the pedigree. This test gave evidence for significant genetic heterogeneity whether the three large pedigrees with seven or more informative males ($P<0.005$), the eight pedigrees with three informative males ($P<0.001$), or all 16 pedigrees ($P<0.001$) were included in the analysis. Second, Morton's large sample test was employed. Significant heterogeneity was present when the analysis was restricted to the three large pedigrees ($P<0.025$), or to the eight pedigrees with informative males ($P<0.05$) but not when smaller, less informative pedigrees were also included. **Third**, an 'admixture' test for heterogeneity was employed which tests for linkage versus no linkage. A trend toward significance was seen ($0.05<P<0.10$) which increased when the analysis was restricted to the larger, more informative pedigrees. The pedigrees where nonpenetrant males are **detected** appear to constitute one class (NP) where tight linkage to factors IX is predicted. The pedigrees where full penetrance is present appear to constitute a second class (P) where loose linkage to factor IX is predicted. Either the chromosomal location of the **mutation** or suppression of recombination to nearby genes may be different in the two classes of pedigrees. In the NP class of fra X predigrees, information from DNA analysis should be useful for carrier **detection**, prenatal **diagnosis**, and genetic counseling.

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ANSWER 1 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:649846 CAPLUS
DOCUMENT NUMBER: 138:11896
TITLE: Biosensor detection of triplex formation by modified oligonucleotides
AUTHOR(S): Bates, Paula J.; Reddoch, James F.; Hansakul, Pintusorn; Arrow, Amy; Dale, Roderic; Miller, Donald M.
CORPORATE SOURCE: Department of Medicine, James Graham Brown Cancer Center, University of Louisville, Louisville, KY, USA
SOURCE: Analytical Biochemistry (2002), 307(2), 235-243
CODEN: ANBCA2; ISSN: 0003-2697
PUBLISHER: Elsevier Science
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Due to the instability of DNA oligonucleotides in biol. solns., antisense or antigene therapies aimed at modulation of specific gene expression will most likely require the use of oligonucleotides with modified backbones. Here, we examine the use of a surface plasmon resonance biosensor (BIAcore) to compare triplex-directed binding of modified oligonucleotides targeted to a region of the murine c-myc promoter. We describe optimization of exptl. conditions to minimize nonspecific interactions between the oligonucleotides and the sensor chip surface, and the limitations imposed by certain backbones and sequence types. The abilities of pyrimidine oligonucleotides with various modified backbones to form specific triple helixes with an immobilized **hairpin duplex** were readily determined using the biosensor. Modification of the **third**-strand **oligonucleotide** with RNA or 2'-O-Me RNA was found to enhance triplex formation, whereas phosphorothioate or phosphotriester substitutions abrogated it. A comparison of these results to DNase I footprinting expts. using the same oligonucleotides showed complete agreement between the two sets of data.

REFERENCE COUNT: 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1999:732986 CAPLUS
DOCUMENT NUMBER: 131:347456
TITLE: Invasive **cleavage** of nucleic acids with thermostable 5'-nuclease for **mutation detection** and **diagnostic** applications.
INVENTOR(S): Prudent, James R.; Hall, Jeff G.; Lyamichev, Victor I.; Brow, Mary Ann D.; Dahlberg, James E.
PATENT ASSIGNEE(S): Third Wave Technologies, Inc., USA
SOURCE: U.S., 182 pp., Cont.-in-part of U.S. Ser. No. 682,853.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 22
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5985557	A	19991116	US 1996-756386	19961126
US 5846717	A	19981208	US 1996-599491	19960124
US 6001567	A	19991214	US 1996-682853	19960712
US 6090606	A	20000718	US 1996-758314	19961202
US 6090543	A	20000718	US 1996-759038	19961202
CA 2243353	AA	19970731	CA 1997-2243353	19970122
WO 9727214	A1	19970731	WO 1997-US1072	19970122
W: AU, CA, JP, US				

RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
AU 9718364 A1 19970820 AU 1997-18364 19970122
AU 731062 B2 20010322
EP 904286 A1 19990331 EP 1997-903931 19970122
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI
JP 2002515737 T2 20020528 JP 1997-526989 19970122
US 5994069 A 19991130 US 1997-823516 19970324
US 6348314 B1 20020219 US 1999-350309 19990709
US 6458535 B1 20021001 US 1999-350597 19990709
US 2004018489 A1 20040129 US 2001-864426 20010524
US 2003044796 A1 20030306 US 2001-940244 20010827
US 6692917 B2 20040217
US 2003096245 A1 20030522 US 2001-982667 20011018
US 2002187486 A1 20021212 US 2001-33297 20011102
US 2002197623 A1 20021226 US 2002-81806 20020222
US 2003186238 A1 20031002 US 2002-84839 20020226
US 2003152971 A1 20030814 US 2002-290386 20021107
US 2004214174 A1 20041028 US 2002-309584 20021204
US 2004072182 A1 20040415 US 2003-356861 20030203
PRIORITY APPLN. INFO.: US 1996-599491 A2 19960124
US 1996-682853 A2 19960712
US 1995-381212 A2 19950131
US 1996-756038 B2 19961126
US 1996-756386 A2 19961126
US 1996-758314 A2 19961202
US 1996-759038 A2 19961202
WO 1997-US1072 W 19970122
US 1997-823516 A1 19970324
WO 1998-US5809 W 19980324
US 1999-350309 A2 19990709
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US 2000-381212 A2 20000208
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US 2000-713601 A2 20001115
US 2000-732622 A2 20001208
US 2001-758282 A2 20010111
US 2001-864636 A2 20010524
US 2001-982667 A1 20011018
US 2001-344946P P 20011107
US 2002-361060P P 20020227
US 2002-290386 A2 20021107

AB The present invention relates to means for the **detection** and characterization of **nucleic acid** sequences, as well as variations in **nucleic acid** sequences. The present invention also relates to methods for forming a **nucleic acid cleavage** structure on a **target sequence** and cleaving the **nucleic acid cleavage** structure in a site-specific manner. The structure-specific 5'-nuclease activity of a variety of enzymes is used to cleave the **target**-dependent **cleavage** structure, thereby indicating the presence of specific **nucleic acid** sequences or specific variations thereof. These 5'-nucleases are capable of cleaving linear **duplex** structures to create single discrete cleavage products identified using fluorescence imaging. The reaction involves a trigger and a detection reaction where a **hairpin** conformation is recognized. Here the target nucleic acid is not completely complementary to at least one of the first, second, **third** and fourth oligonucleotides. Assays where the **target nucleic acid** is reused or recycled during multiple rounds of hybridization with **oligonucleotide** probes and **cleavage** without the need to use temperature cyclin or

nucleic acid synthesis. Through the interaction of the **cleavage** means an upstream **oligonucleotide** can be made to cleave a downstream **oligonucleotide** at an internal site in such a way that the resulting fragments of the downstream **oligonucleotide** dissociated from the **target nucleic acid**, thereby making that region of the **target nucleic acid** available for hybridization to another, uncleaved copy of the downstream **oligonucleotide**. The specific stability designed into the invader and **probe** sequences will depend on the temperature at which one desires to perform the reaction. It is desirable that the invader **oligonucleotide** be immediately available to direct the **cleavage** of each **probe** **oligonucleotide** that hybridizes to a **target nucleic acid**. For this reason, the invader **oligonucleotide** is provided in excess over the **probe** **oligonucleotide**. The non-**target cleavage** products are incubated with a template-independent polymerase and one nucleoside triphosphate under conditions such that at least one nucleotide is added to the 3'-hydroxyl group of the non-**target** **cleavage** products to generate tailed products. The present invention also provides novel methods and devices for the separation of nucleic acid mols. by charge by charge reversal. When an **oligonucleotide** is shortened through the action of a CLEAVASE enzyme or other cleavage agent, the pos. charge can be made to not only significantly reduce the net neg. charge, but to actually override it, effectively "flipping" the net charge of the labeled entity. The reversal of charge allows the products of **target**-specific **cleavage** to be partitioned from uncleaved **probe** by extremely simple means. It has clin. diagnostic applications as multiple alleles could be screened at once.

REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 3 OF 4 EMBASE
on STN

ACCESSION NUMBER: 96015026 EMBASE
DOCUMENT NUMBER: 1996015026
TITLE: Conformations of three-stranded DNA structures formed in presence and in absence of the RecA protein.
AUTHOR: Dagneaux C.; Porumb H.; Liquier J.; Takahashi M.; Taillandier E.
CORPORATE SOURCE: Laboratoire CSSB URA CNRS 1430, UFR SMBH, Universite Paris, 74, rue Marcel Cachin,F-93012 Bobigny Cedex, France
SOURCE: Journal of Biomolecular Structure and Dynamics, (1995) 13/3 (465-470).
ISSN: 0739-1102 CODEN: JBSDD6
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Using FTIR and UV spectroscopies, we have studied the structures of three-stranded DNA complexes (TSC) having two identical strands, containing all four bases, in parallel orientation. In the first system, an intermolecular TSC is formed by the addition of the **third** strand (ssDNA) previously coated with RecA protein to an **hairpin** **duplex** (dsDNA), in presence of ATPγS. In the second one, the formation of an intramolecular triplex is forced by folding back twice on itself an **oligonucleotide**. The sequences of the three strands are the same in both systems. The formation of the RecA-TSC, which accommodates all four bases, is evidenced by gel retardation assay, and by its biphasic melting profile observed by UV spectroscopy. Using FTIR

spectroscopy, N-type sugars are **detected** in this structure. This shows that in the RecA-TSC studied in presence of the protein, the **nucleic acid** part adopts an extended form, in agreement with the model proposed by Zhurkin et al. (1,2) and electron microscopy observations (3-6). In contrast, the RecA- free intramolecular triplex in a non extended form has S-type sugars.

L12 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1995:38082 CAPLUS
DOCUMENT NUMBER: 122:181133
TITLE: A base-triplet model for homologous recognition promoted by RecA protein
AUTHOR(S): Rao, B. J.; Chiu, S. K.; Radding, C. M.
CORPORATE SOURCE: School Medicine, Yale University, New Haven, CT, 06510, USA
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AB RecA protein formed a stable triple-stranded joint from a **hairpin duplex oligonucleotide** and single-stranded M13 DNA. In the deproteinized triple-stranded DNA joints, the complementary strand of the **hairpin** substrate remained paired with the incoming single-strand and formed a **duplex** substructure. However, the non-complementary (**third**) strand revealed properties consistent with a novel triplex structure: (i) this strand exhibited novel sites of **cleavage** by DNase I, found neither in single-strand nor in **duplex** controls (ii) resisted **cleavage** by E. coli exonuclease I in the conditions where a control single-strand of the same **sequence** was sensitive (iii) most of its purine residues, especially adenines, were hyperreactive to KMnO4 modification in the conditions where KMnO4 exhibited normal specificity by modifying only thymine residues in control single-strands. Moreover, the enzymic methylation in the major-groove of only two N-6 adenines and two N-4 cytosines in the **hairpin** substrate prior to the pairing destabilized the triplex more severely than the control **duplex** of the same size and sequence. A triplex-model has been proposed to rationalize the results. The planar base triads hint at the role of putative non-Watson-Crick motifs in RecA- mediated homologous recognition. Results from a sep. set of reactions involving RecA presynaptic filaments and single-stranded oligonucleotides strengthened this proposal by revealing that RecA filaments can recognize homol. via non-Watson-Crick motifs.

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